

EXHIBIT IV



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.16 [Mar-25-2007]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.0000 wordsize: 3 Filter ☒ View option Mismatch-highlighting

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation**Sequence 1:** lcl|seq_1

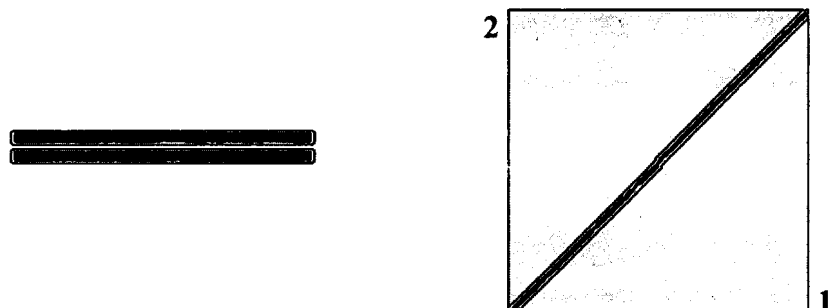
Length = 836 (1 .. 836)

Sequence 2: gi|14328879|gb|AAK02058.1|CUB domain containing protein 1 [Homo sapiens]

>gi|119585141|gb|EAW64737.1| CUB domain containing protein 1, isoform CRA_a [Homo sapiens]

>gi|119585142|gb|EAW64738.1| CUB domain containing protein 1, isoform CRA_a [Homo sapiens]

Length = 836 (1 .. 836)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1556 bits (4030), Expect = 0.0
Identities = 834/836 (99%), Positives = 836/836 (100%), Gaps = 0/836 (0%)

| | | | |
|-------|-----|---|-----|
| Query | 1 | MAGLNCGVSIALLGVLLLGAARLPRGAFAFEIALPRESNITVLIKLGTPDLLAKPCYIVI | 60 |
| Sbjct | 1 | | 60 |
| Query | 61 | SKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMGPCPFGEVQLQPSTSLIPT | 120 |
| Sbjct | 61 | | 120 |
| Query | 121 | LNRTFIWDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSN | 180 |
| Sbjct | 121 | | 180 |
| Query | 181 | GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY | 240 |
| Sbjct | 181 | | 240 |
| Query | 241 | PEGFPEDELMTWQFVVPAPHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDK | 300 |
| Sbjct | 241 | | 300 |
| Query | 301 | QPGNMAGNFNLSLQGCDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIE | 360 |
| Sbjct | 301 | | 360 |

```
Query 361 PRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDH 420
Sbjct 361 ..... 420

Query 421 RYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQQHTHEKPCNTSF 480
Sbjct 421 ..... 480

Query 481 SYLVASAIPSQDLYFGSFCPGGSIKQIQVKQNISVTLRTFAPSFQEQASRQGLTVSFIPY 540
Sbjct 481 .....Q..... 540

Query 541 FKEEGVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFFKERSGVVCQ 600
Sbjct 541 ..... 600

Query 601 TGRAFMIIQEQRTRAEEIFSLDEDVLPKPSFHHHSFWVNISNCSPTSGKQLDLLFSVTLT 660
Sbjct 601 ..... 660

Query 661 PRTVDLTVILIAAVGGGVLLLSALGLIICCVKKKKKKTNKGPAVGIYNGNINTEMPRQPK 720
Sbjct 661 ..... 720

Query 721 KFQKGRKDNDSHVYAVIEDTMVYGHLLQDSSGSFLQPEVDTYRPFQGTMGVCPSPPTIC 780
Sbjct 721 ..... 780

Query 781 SRAPTAKLATEEPPPRSPPESESEPYTFSHPNNGDVSSKDTDIPLLSTQEPMEPAE 836
Sbjct 781 .....N..... 836
```

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.